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ABSTRACT

The Northern North Carolina Estuarine System (NNCES) stock of the common bottlenose dolphin (*Tursiops truncatus*) has a small population size and low Potential Biological Removal level (PBR). Levels of serious injury and mortality due to commercial fisheries interactions may exceed the PBR. In addition, the prior abundance estimate, from a survey in 2006, is no longer valid for computing the PBR for the stock after 2014. To obtain a new abundance estimate, we conducted a capture-mark-recapture survey of the NNCES stock in the Pamlico-Albemarle Estuarine Complex (PAEC) from 15 June to 27 July 2013. The PAEC is the primary summer habitat for the stock. We surveyed 4,779 km of trackline, encountering 128 dolphin groups. We took 30,991 photographs, from which 471 individual dolphins were identified from distinctive nicks and notches on dorsal fins. Because dolphins in the most southern portion of the summer habitat overlap with the Southern North Carolina Estuarine System (SNCES) stock in July, some photographed dolphins could have been members of the SNCES stock. We developed a decision tree to identify dolphins that may have belonged to the SNCES stock, thereby allowing us to estimate abundance using all dolphins and then excluding those that might belong to the SNCES stock. We then calculated lower (823; 95% posterior interval (PI) = 733-931) and upper (873; 95% PI = 775-989) bounds on the abundance estimate based on habitat-use assumptions from the decision tree. Both estimates were obtained using closed capture-mark-recapture models and a novel method to correct for dolphins with indistinctive fins.

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INTRODUCTION

Marine mammal stocks with small population sizes are especially vulnerable to anthropogenic impacts. Current and accurate population abundance estimates, therefore, are critical to the conservation of these stocks by determining if estimated levels of serious injury and mortality are above/below sustainable levels (i.e., Potential Biological Removal level [PBR]; Marine Mammal Protection Act [MMPA], 16 U.S.C. 1362 [20]; Wade and Angliss 1997). Two estuarine common bottlenose dolphin (*Tursiops truncatus*) stocks occur in estuarine waters of North Carolina (NC) and both have low abundances and PBRs: the Northern North Carolina Estuarine System (NNCES) and the Southern North Carolina Estuarine System (SNCES) stocks (Waring et al. 2014). Levels of serious injury and mortality due to commercial fisheries interactions (i.e., bycatch) may exceed PBR (Waring et al. 2014). The prior abundance estimates for both stocks were estimated from surveys conducted in 2006 (Urian et al. 2013) and will no longer be valid after 2014 for computing the PBR (Wade and Angliss 1997). Of the two estuarine stocks in NC, bycatch was thought to be greater for the NNCES stock and updating the abundance estimate for this stock was given priority in 2013 over the SNCES stock.

The purpose of this report is to provide that new abundance estimate for the NNCES stock. The NNCES stock is parapatric with the SNCES stock and two migratory stocks of common bottlenose dolphins that also occur in NC. The spatiotemporal scope of the study, therefore, was chosen to decrease the likelihood that dolphins were from these other stocks on the basis of prior information used to define stock boundaries for the Stock Assessment Report (Waring et al. 2014). The sampling method followed recommendations from a workshop that identified best capture-mark-recapture (CMR) methodology for using photo-identification surveys to estimate abundance of common bottlenose dolphins in bays, sounds and estuaries of the US east coast and Gulf of Mexico coasts (Rosel et al. 2011).

METHODS

Spatial and Temporal Coverage of Surveys

During the summer, the NNCES stock occurs primarily in the Pamlico-Albemarle Estuarine Complex (PAEC) (Epperly and Ross 1986, Fig. 1) with limited spatiotemporal overlap of the SNCES and southern migratory stocks (Waring et al. 2014). Actual or potential overlap with individuals from the SNCES stock occurs inshore during July in the most southern extent of the NNCES stock inshore range. Similarly, overlap with the southern migratory stock occurs in nearshore coastal waters during July through September. Therefore, the photo-identification surveys began in June and excluded all nearshore coastal waters and portions of the inshore southern extent of the NNCES stock range (i.e. Bogue Sound, North River, and the most southern portion of Core Sound).

Using ArcGIS 10, tracklines were created to follow the inshore coastline of the PAEC and a portion of the open-water area in Albemarle and Pamlico Sounds (Figs. 1, 2a). The tracklines were intended as a guide for daily surveys because they were created without taking into account exact water depths and shifting channels. The tracklines were divided into sections (average 49.6 km [range: 21-70 km]) that could be completed in a day. Planned coordinates at

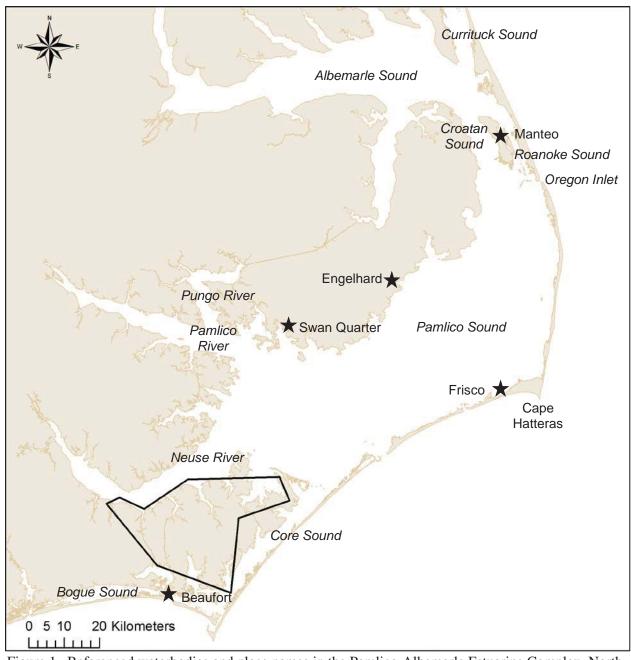


Figure 1. Referenced waterbodies and place names in the Pamlico-Albemarle Estuarine Complex, North Carolina (NC). Manteo is on Roanoke Island, between Croatan and Roanoke Sounds. The black polygon indicates the area where animals assigned to the Southern NC Estuarine System stock have been documented in July from prior telemetry or photo-identification studies (Waring et al. 2014).

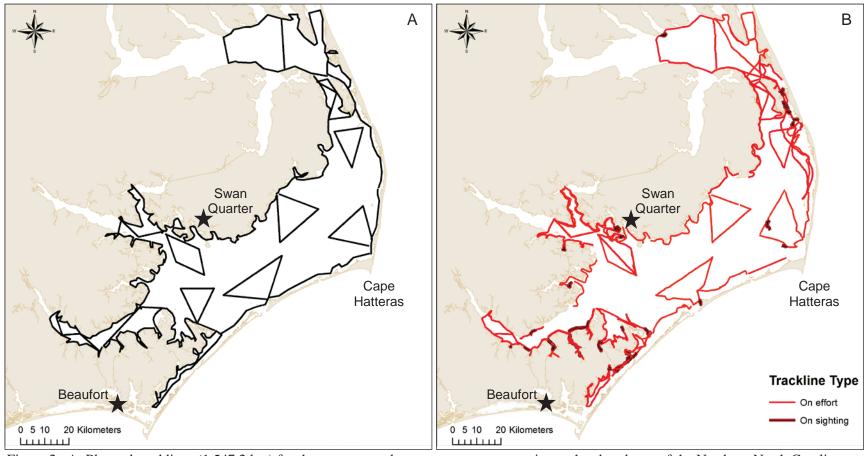


Figure 2. A: Planned tracklines (1,547.2 km) for the capture-mark-recapture survey to estimate the abundance of the Northern North Carolina Estuarine System Stock. B: Actual vessel tracklines surveyed during the "capture-mark" session (15-27 June) separated into on effort (red lines; 2,096.7 km) and on sighting (red/black lines; 169.1 km).

the beginning and end of each section and at direction changes along the sections were extracted from ArcGIS and end of each section and at direction changes along the sections were extracted from ArcGIS and uploaded into each boat's GPS. Transects did not cover the entire portions of the Neuse River and the Albemarle and Currituck Sounds because encounters were unlikely due to very low salinity and lack of historical sightings/strandings of bottlenose dolphins (Gannon 2003, Byrd et al. 2014).

Data collection

Surveys were conducted in accordance with the Best Practices recommendations from Rosel et al. (2011) with the exception that they focused on one season. The surveys comprised three capture-mark-recapture sessions from 15 June to 27 July 2013, with seven days between sessions. For the first session (the "mark") the entire inshore habitat of the NNCES stock, except as noted above, was systematically surveyed, rather than focusing exclusively in areas of high density. The mark required three teams (northern, central, and southern) surveying from 15-27 June for full coverage of all tracklines. The northern team was based in Manteo, NC, and surveyed Albemarle, Croatan, and Roanoke Sounds, as well as the northern section of Pamlico Sound (Figs. 1, 2a). The central team was based in Frisco, NC, for the first week, surveying the central and eastern sections of Pamlico Sound. For the second week, it was based in Engelhard, NC, and surveyed the central and western sections of Pamlico Sound and Pamlico River. The southern team was based in Beaufort, NC, and surveyed Core Sound, the Neuse River, and the southern section of Pamlico Sound. For the second and third sessions ("recaptures"), areas where no dolphins were found during the initial capture session were excluded to increase the recapture efficiency. Only the northern and southern teams were needed for the two recapture sessions. The recapture sessions extended for approximately one week: the first from 6-14 July and the second from 20-27 July.

Surveys were conducted primarily in Beaufort sea-state scale of 3 or less. The northern team used a 6-m rigid-hull boat with a 150 hp outboard engine during the mark session and 6.7m rigid-hull inflatable boat with two 90-hp outboard engines during the recapture sessions, which was used by the central team during the mark session. The southern team used a 5.5-m rigid hull boat with a 115 hp outboard engine during the entire study. All boats were driven at 10-14 knots when on effort. Each team consisted of a boat operator, a primary and secondary photographer, and a data recorder. For the central vessel, the secondary photographer also was the data recorder. Time and geographic coordinates were recorded when the surveys were on or off effort, when the boat was following a dolphin sighting ("on sighting"), and when Beaufort sea-state scale changed. Photographs of dorsal fins were taken with either a Canon 40D or 20D digital SLR camera using 100-300 mm lenses. When dolphins were sighted, the boat was maneuvered parallel to the animals to minimize disturbance. Geographic coordinates for the sighting were recorded using a GPS when the boat approached the dolphins rather than at the boat's position when the sighting first occurred because some sightings were made at a distance. Photographers were instructed to photograph dorsal fins of all dolphins regardless of fin distinctiveness or whether or not the animal had already been photographed within the sighting (or day) to not bias effort of photographing only well-marked individuals (Eguchi 2014). Sightings typically ended when all dolphins were photographed. During the mark session, however, a time limit of one hour was imposed to ensure that tracklines could be completed. At the end of each sighting, geographical position, group size, depth, sea state, and salinity were

recorded. If the depth varied greatly throughout the sighting, the estimated median depth was recorded. Each GPS was programmed to automatically record a geographic position every 30 seconds to document the actual trackline.

Photographic processing

All photographs from sightings were sorted by individual dolphin. Photo quality and distinctiveness were determined for each dolphin from each sighting. The best photograph of each dolphin from each sighting was assigned a photographic quality rating of poor, fair, good or excellent based on focus, size, and angle of the dorsal fin (Baird et al. 2008). Dorsal fins were also assigned a distinctiveness rating of not distinctive, slightly distinctive, distinctive, or very distinctive (Baird et al. 2008). Images with photographic quality of good or excellent and distinctiveness rating of distinctive or very distinctive were used in the analysis. We also included in the analysis images scored as slightly distinctive with photographic qualities of excellent because we assumed that unique features would not change during the short duration of our study. Images of individual dolphins were entered into Finscan 1.6.2 (Hillman et al. 2003), which was used to assist in matching individual dolphins between sightings across the three sampling sessions. Matches were reviewed and agreed upon by two experienced researchers and all identified dolphins were compared to all images in the catalogue to ensure that no matches were missed.

Mark-recapture analysis

As stated above, the PAEC area surveyed includes habitat where SNCES stock dolphins have also been documented in July. As such, we created a polygon, using ArcGIS, around the area of overlap of both stocks using stock definition information provided in Waring et al. (2014) (Fig. 1). Then we developed a decision tree with criteria based on habitat-use assumptions to objectively identify individuals in the polygon with a high probability of belonging to the NNCES stock versus the SNCES stock (Table 1). With this information, two abundance estimates were generated, representing a likely upper bound (all dolphins in the area of spatiotemporal overlap except those affirmatively identified as SNCES stock) and lower bound (includes only those dolphins affirmatively classified as NNCES stock).

Abundance was estimated using closed capture-mark-recapture models. The assumption of closure of the stock for the study period is supported by movement records from satellite telemetry (Hohn and Hansen, unpub. data; Waring et al. 2014) and other photo-identification results (Waring et al. 2014). Because of the short duration of the sampling and the high survival rates of non-calves (Scott et al. 1990), we assumed that no deaths occurred in the stock during the study. Due to the large sampling area, even with three independent teams operating simultaneously, the entire study area could not be sampled in one day. Consequently, we pooled all survey days within each session.

A total of seven CMR models were fitted to resighting histories of dolphins (Table 2). These models differ in the underlying assumptions. We used the data augmentation approach to estimate abundance through the CMR models (Royle et al. 2007, Kéry and Schaub 2012).

Table 1. For the spatiotemporal scope of the study, the decision tree used to identify dolphins that likely belong to the NNCES stock or could have been belonged to either the NNCES or SNCES stocks. See Fig. 1.

Stock Assignment	Criterion		
NNCES	In Pamlico Sound, Albemarle Sound, and all inclusive tributaries and sounds except for the Neuse River		
	In Core Sound except for the southern-most portion included in the polygon of overlap (Fig. 1)		
	Along the northern shore of the Neuse River		
	In overlap polygon in June, which includes the southern shoreline of the Neuse River and the southernmost portion of Core Sound		
	Freeze-branded animals previously assigned to stock based on sighting histories		
NNCES or SNCES In overlap polygon (Fig. 1) in July, which includes the southern sho the Neuse River and the southernmost portion of Core Sound			
SNCES	Freeze-branded animals previously assigned to stock based on sighting histories		

Table 2. Descriptions of capture-mark-recapture models used.

Model	Description			
M0	This is the simplest model for which sighting probability of dolphins is assumed constant over time and among dolphins			
Mt	Sighting probability is assumed to vary among samples, perhaps because of weather and other conditions			
Mb	Sighting probability is assumed to change between the first and subsequent captures due to the change in behavior of animals. This assumption probably does not apply to photographic captures. When animals are caught physically, depending on how they are trapped, they may get trap-happy or trap-shy, resulting in change in the capture probability after the first capture			
Mh	This model is based on the assumption that each individual has its own sighting probability (capture heterogeneity). We treat this heterogeneity as individual random effects rather than using covariates			
Mth	Time and individual effects on sighting probability are combined in this model. In this analysis, time effects are treated as additive fixed effects whereas capture heterogeneity is treated as individual random effects			
Mtb	Time and behavioral effects on sighting probability are combined in this model. Not only there is a difference in first and subsequent captures, they are also changed over time			
Mtbh	This model combines all three factors, i.e., time, behavioral, and capture heterogeneity, that may affect the sighting probability			

Photographic capture-recapture analyses only provide abundance estimates for those individuals that can be identified (N_{marked}). To estimate the total abundance, including those that cannot be identified (often due to unmarked fins), we used the method described in Eguchi (2014). The method uses repeated sampling of individuals in groups to estimate the proportion of identifiable animals (θ). The total abundance (N_{total}) is estimated simply ($\hat{N}_{marked}/\hat{\theta}$), where a "hat" indicates an estimate. Both analyses, i.e. N_{marked} and θ , were conducted simultaneously.

We used flat prior distributions for the majority of the parameters in the models except the precision parameter for the sighting probabilities in the individual random effects models (i.e., M_h , M_{th} , and M_{tbh} models). We used a gamma distribution (GAM(5, 1)) as the prior distribution for the precision parameter, which improved the convergence of the analysis. The GAM(5, 1) distribution has 95% of its density between 1.6 and 10.2, which corresponds to the variance between 0.1 and 0.6. We think that range was broad enough for the parameter. Note that with three capture occasions models that include individual capture heterogeneity parameters can produce unreliable estimates (Conn et al. 2006). We compared the prior and posterior distributions of the parameter to determine if the data were informative for this parameter. If data were not informative, posterior and prior distributions would be similar or identical.

For each analysis (a combination of model and dataset), 100,000 steps of five independent chains were used to tune the MCMC (Markov Chain Monte Carlo) and the same numbers of steps and chains were used to obtain samples from the joint posterior distribution. Chains were not thinned, following the recommendation by Link and Eaton (2012). These 500,000 samples were used to compute summary statistics for each parameter. To select the best model among the seven, we used the deviance information criteria (DIC = the mean deviance + posterior variance of deviances × 1/2; Spiegelhalter et al. 2002, Gelman et al. 2014). Summary statistics are provided in the mean and 95% posterior intervals (PI). All analyses were conducted using JAGS (v. 3.3.0; Plummer 2012) via the rjags package (v. 3.13; Plummer 2014) and R (v. 3.0.2 and v. 3.1.0; R Development Core Team 2014). R and JAGS code used in this study are available in the Appendices.

RESULTS

Across all three sampling sessions, 258.8 hours of survey time on effort covered 4,778.9 km of trackline (Table 3, Figs. 2b, 3). When poor conditions prevented surveying part of the trackline, we returned to that area on another day. A total of 128 dolphin groups were recorded (Fig. 4), including 12 neonates and 83 young-of-year. Group sizes ranged from 1 - 55 (mean = 10.1). Dolphins were encountered in water depths of 0.3 - 8.5 m (mean = 1.9 m) with the sighting at 8.5 m found at the Oregon Inlet bridge (Fig. 1). Salinity ranged from 1.90 - 36.80 ppt. The lowest salinity was found on the north side of Albemarle Sound and many of the dolphins in these sightings exhibited lesions assumed to be associated with extended exposure to freshwater (e.g. Hart et al. 2012) (Fig. 5).

Photographs (n = 30,991) were available from 124 out of 128 dolphin groups. There were 961 identifications with 597 unique individuals across all qualities and distinctive ratings,

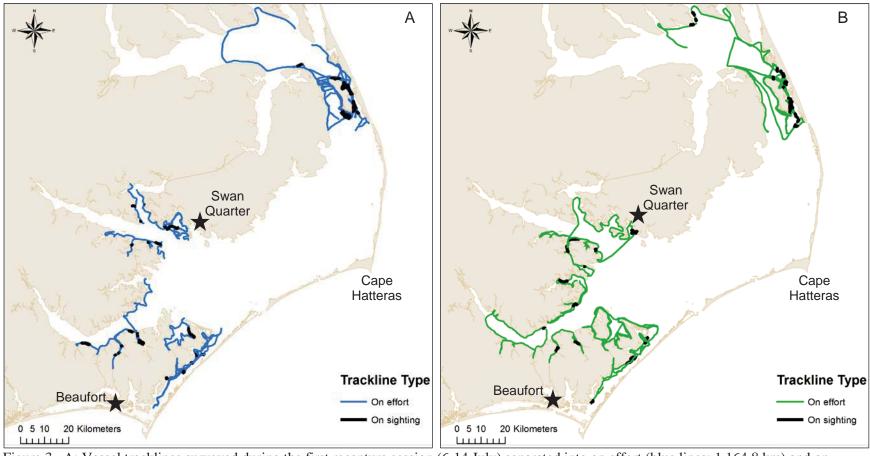


Figure 3. A: Vessel tracklines surveyed during the first recapture session (6-14 July) separated into on effort (blue lines; 1,164.8 km) and on sighting (blue/black lines; 129.0 km). B: Vessel tracklines surveyed during the second recapture session (20-27 July) separated into on effort (green lines; 1,517.4 km) and on sighting (green /black lines; 109.8 km).

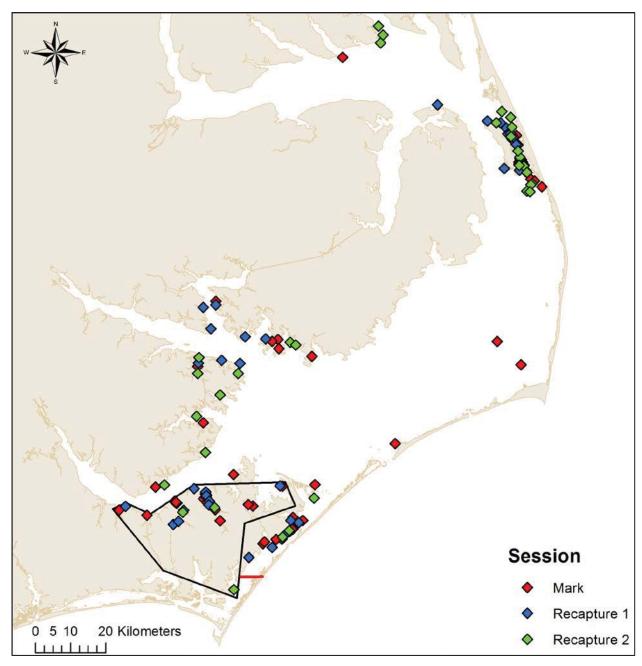


Figure 4. Dolphin sightings (at initial sighting location) during the capture-mark-recapture survey to estimate the abundance of the Northern North Carolina Estuarine System (NNCES) stock, June-July 2013. The black polygon indicates the area where animals assigned to the Southern North Carolina Estuarine System (SNCES) stock have been documented in July from prior telemetry or photo-identification studies (Waring et al. 2014). The red line in southern Core Sound is the boundary used by Read et al. (2003) and Urian et al. (2013) to assign sightings to the NNCES stock (north of the line) or to the SNCES stock (south of the line).

Table 3. Summary of effort for each session and overall of the capture-mark-recapture project in summer 2013. An asterisk (*) denotes that the number of unique dolphins (all photo and distinctiveness qualities) across all sessions does not equal the sum of numbers for each session because each session includes animals that were resightings.

	Mark	Recapture 1 Recapture 2		Across
	15-27 June	6-14 July	20-27 July	periods
On effort trackline (km)	2,097	1,165	1,517	4,779
On sighting trackline (km)	169	129	110	408
Off effort trackline (km)	1,068	275	143	1,486
# of sightings	55	41	32	128
# of photos	9,206	8,219	13,566	30,991
# of unique dolphins	235	142	220	471*

Table 4. Estimated parameters, deviances, and DIC values for the capture-mark-recapture models. N_{marked} indicates the abundance of identifiable dolphins and N_{total} indicates the abundance of dolphins including unmarked fins. Point estimates are means and uncertainties are 95% posterior intervals (PI). Bold letters indicate the model and estimates with the lowest DIC values. Lower and Upper indicate the two datasets for the lower and upper bounds on abundance estimates as described in the text.

Models		Deviance (SD)	DIC	N _{marked} [95% PI]	N _{total} [95%PI]
M_0	Lower	6108.3 (85.0)	9717.0	834 [741, 945]	846 [750, 958]
	Upper	6228.6 (87.3)	10042.4	885 [784, 1004]	897 [795, 1018]
M	T	(020.0 (02.6)	0525.5	012 [724 010]	022 [#22 021]
\mathbf{M}_{t}	Lower	6039.9 (83.6)	9535.7	812 [724, 918]	823 [733, 931]
	Upper	6159.5 (86.9)	9937.1	862 [765, 975]	873 [775, 989]
M_b	Lower	6074.2 (115.5)	12748.1	815 [696, 971]	826 [705, 985]
Ü	Upper	6216.4 (116.4)	12987.6	879 [746, 1033]	890 [756, 1047]
$\mathrm{M_{h}}$	Lower	5190.6 (87.0)	8972.6	951 [811, 1154]	964 [822, 1170]
	Upper	5277.6 (90.1)	9340.9	1010 [857, 1205]	1024 [868, 1222]
M_{tb}	Lower	6198.9 (128.7)	14484.4	923 [766, 1138]	936 [776, 1154]
TVIED	Upper	6331.0 (131.9)	15035.2	986 [815, 1214]	999 [826, 1231]
	* *				
M_{th}	Lower	6092.4 (88.3)	9988.6	917 [785, 1112]	930 [796, 1127]
	Upper	6218.0 (92.3)	10479.2	977 [833, 1189]	990 [844, 1205]
	_				
$ m M_{tbh}$	Lower	6214.0 (124.4)	13951.5	1008 [818, 1260]	1022 [829, 1278]
	Upper	6349.2 (124.5)	14079.5	1079 [875, 1324]	1094 [886, 1341]



Figure 5. Example of dolphins photographed in the Albemarle Sound with skin lesions assumed to be associated with extended exposure to low-salinity water (e.g. Hart et al. 2012).

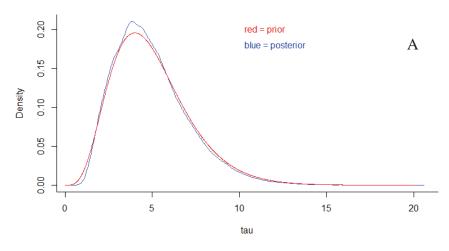
including three freeze-branded dolphins previously assigned to the SNCES stock (Garrison, personal commun.), one of which was seen in June. After removing the known SNCES stock animals and the individuals that did not meet our distinctiveness and photographic quality criteria, 683 identifications and 471 unique individuals remained for the capture-mark-recapture analysis for the upper bound abundance estimate (Table 3). Of these, 334 individuals were sighted only once. For the lower bound estimate, 14 dolphins in the polygon that could not be affirmatively assigned to either the NNCES or SNCES stock were removed from the analysis.

Abundance estimates

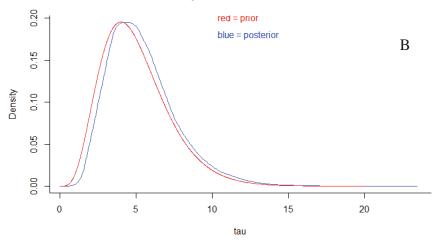
Convergence was reached for all model and dataset combinations based on the Gelman-Rubin statistic, where all Rhat statistics were less than 1.1 (Gelman et al. 2014). Although the comparison of DIC among the models indicated M_h was the best model (Table 4), posterior distributions of the random-effects parameter (tau) were similar to the prior (GAM(5, 1), Fig. 6), indicating data were not informative for this parameter. Consequently, we discarded the results from these models (M_h , M_{th} , M_{tbh}). Among the remainder of the models, M_t was the best according to the DIC values (Table 4). Marginal posterior distributions of N_{marked} and N_{total} were symmetric and no signs of truncated tails indicated that posterior samples represented the entire posterior distributions (Kéry and Schaub 2012). The mean abundance (N_{total}) for the lower bound was 823 (95%PI = 733-931, CV = 0.06); whereas, that for the upper bound was 873 (95%PI = 775-989, CV = 0.06) (Table 4).

Figure 6. Comparison of prior and posterior distributions for the tau parameter, which is the precision of capture heterogeneity. A: M_h , B: M_{th} , C: M_{tbh}

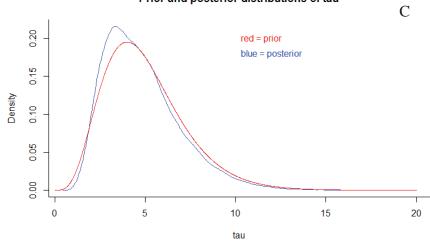
Prior and posterior distributions of tau



Prior and posterior distributions of tau



Prior and posterior distributions of tau



DISCUSSION

This study updates the expiring abundance estimate for the NNCES stock and establishes a decision tree for how to approach the known spatial overlap of the NNCES and SNCES stocks in the study area during July. The lower and upper bound estimates were similar to each other with overlapping 95% PIs; the lower bound estimate likely excluded SNCES stock animals and some unknown numbers of NNCES stock animals. Eliminating the individual random effects would decrease the abundance estimate, which would provide a more conservative abundance estimate. More than five sampling occasions are probably necessary to estimate this parameter (Conn et al. 2006).

The abundance estimates for the NNCES stock obtained from this study (823-873) were similar to the previous two estimates from 2000 (919, 95% CI 730-1190, CV = 0.13, Read et al. 2003) and 2006 (950, 95% CI 516-1384, CV = 0.23, Urian et al. 2013). These similarities are despite the differences in the sampling design and the analyses. For example, prior studies included animals that occurred in the polygon area in July (Fig. 1), which may have included SNCES stock dolphins, similar to our approach for the upper estimate. Other differences between prior studies and this study include: (1) previous studies calculated the number of unmarked animals by dividing the population estimate by θ (counting the proportion of marked to unmarked animals), whereas we estimated the proportion using a statistical model and appropriate sampling method, (2) previous studies included surveys of coastal waters out to 1 km; whereas our study was limited to inshore waters of PAEC, which reduced the probability of including individuals from the coastal Southern Migratory stock, 3) previous studies surveyed only "hot spots" during the mark session, whereas we systematically surveyed almost the entire estuarine range of the NNCES stock in summer. "Hot spots" of bottlenose dolphins in the area were based on reports of dolphin sightings by local watermen whose distributions in the area were likely not uniform. The wider survey of the entire range during the mark session, rather than using known hot spots, enabled us to avoid possible sampling bias. Additionally, previous studies used the model M_t to estimate the abundance (Read et al. 2003, Urian et al. 2013) in contrast to our study, where we explored other models that included capture heterogeneity among individuals. Because of the difference in how each fin may be identified due to differences in degrees of distinctiveness, it is likely that capture probabilities vary among individuals. Because of the small number of capture-mark-recapture occasions, however, we could not reliably use models with capture heterogeneity (M_h, M_{th}, and M_{thh}) even though M_h had the lowest DIC value (Table 4). Including this level of variability with sufficient data would increase the estimated abundance. Consequently, the estimates given in this report should be treated as conservative.

We have developed a decision tree to deal with dolphins that can be found in an area where two stocks may coexist. Our approach explicitly deals with the stochastic nature of how dolphins may move within the overlapping area and provide upper and lower abundance estimates. We think the approach provides abundance estimates that reflect our knowledge of stock distributions and, therefore, is better than using a permanent geographic line to delineate the distribution of these two stocks.

This work establishes new abundance estimate for the NNCES stock to replace the expiring estimate. Additional work is needed to better understand and define the spatiotemporal mixing of the NNCES and SNCES stocks, and how to best distinguish between stocks for abundance estimation when considering sampling methods.

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Appendix 1. JAGS code

This code segment is used to estimate the proportion of identifiable individuals. This segment should be inserted into each CMR model below.

```
# for each observed group
for (g in 1:G) {
  for (i in 1:x[g]){
    # the number of photos per individual is Poisson
   k[i,g] ~ dpois(mu[g])
  # exp(-mu[q]) = Pr(not observing the ith animal) with Poisson
  # So, probability of observing x[g] animals in m[g] animals is
  # binomial with 1-exp(-mu[g,j]).
  phi[g] \leftarrow 1 - exp(-mu[g])
 mu[g] \sim dgamma(0.1, 0.1)
  # the number of observed identified individuals in each group is binomial
  # with the total identifiable individuals (m) in the group.
  x[g] \sim dbin(phi[g], m[g]) # ID'd individuals
  # M[g] is the total number of identified individuals using
  # all photo qualities.
  m1[g] ~ dcat(pi)
  m[g] \leftarrow m1[g] + M[g]
  # photographic "efficiency". The total number of usable photographs
  # out of total number of photographs taken is efficiency dependent.
  e[g] ~ dbeta(eAlpha, eBeta)
  T[g] \sim dbin(e[g], N[g]) \# efficiency of photographers
  # p2 is the proportion of identifiable individuals in the group, which
  # is modeled in the logit space.
  logit(p2[q]) \leftarrow eps[q]
  eps[g] ~ dnorm(mean.lp, tau2)
  K[g] ~ dbin(p2[g], T[g]) # Prob of "capture"
  Grp[g] \leftarrow m[g]/p2[g] \# Group size
# priors
tau2 <- 1/(s * s)
s \sim dunif(0, 3)
mean.lp <- logit(mean.p)</pre>
mean.p \sim dunif(0, 1)
eAlpha ~ dunif(1,5)
eBeta \sim dunif(1,5)
```

The following code segments are used to estimate abundance of identifiable dolphins. The previous code segment to estimate the proportion of identifiable dolphins should be inserted into where the following sentence appears: "Insert the proportion of identifiable individual section here." This code can be found in Kéry and Schaub (2012).

```
M0:
# Closed model 1 from Kery and Schaub 2012. p. 142
# M0

model {
    # abundance of marked individuals
```

Appendix 1 continued.

```
# priors
 Omega \sim dunif(0, 1)
 p \sim dunif(0, 1)
  # likelihood
  for (i in 1:I) {
    z[i] ~ dbern(Omega)
    for (j in 1:J){
     yaug[i, j] ~ dbern(p.eff[i,j])
     p.eff[i, j] <- z[i] * p
  N0 <- sum(z[])
  Insert the proportion of identifiable individual section here.
 Ntotal <- N0/mean.p</pre>
Mb:
model {
 # abundance of marked individuals
  # priors
 Omega \sim dunif(0, 1)
 p \sim dunif(0, 1)
  c \sim dunif(0, 1)
  # likelihood
  for (i in 1:I){
   z[i] \sim dbern(Omega)
   # first occasion
   yaug[i, 1] \sim dbern(p.eff[i,1])
   p.eff[i,1] <- z[i] * p
   for (j in 2:J){
      yaug[i, j] ~ dbern(p.eff[i,j])
      p.eff[i, j] \leftarrow z[i] * ((1 - yaug[i, (j-1)]) * p + yaug[i, (j-1)] * c)
  N0 < - sum(z[])
  trap.response <- c - p
  Insert the proportion of identifiable individual section here.
 Ntotal <- N0/mean.p
Mt:
model {
 # abundance of marked individuals
  # priors
 Omega ~ dunif(0, 1)
  for (j in 1:J){
   p[j] \sim dunif(0, 1)
  # likelihood
```

Appendix 1 continued.

```
for (i in 1:I){
    z[i] \sim dbern(Omega)
    for (j in 1:J){
      yaug[i, j] ~ dbern(p.eff[i,j])
p.eff[i, j] <- z[i] * p[j]</pre>
  N0 < - sum(z[])
  Insert the proportion of identifiable individual section here.
  Ntotal <- N0/mean.p2</pre>
Mth:
model {
  # abundance of marked individuals
  # priors
  Omega ~ dunif(0, 1)
  for (j in 1:J){
    mean.lp[j] \leftarrow log(mean.p[j] / (1 - mean.p[j]))
    mean.p[j] \sim dunif(0, 1)
  # changed sd and tau definition to see if
  # defining a prior on tau may help convergence
  tau \sim dgamma(5, 1)
  sd <- 1/sqrt(tau)</pre>
  # likelihood
  for (i in 1:I){
    z[i] \sim dbern(Omega)
    eps[i] ~ dnorm(0, tau)
    for (j in 1:J){
      lp[i,j] <- mean.lp[j] + eps[i]</pre>
      p[i,j] \leftarrow 1 / (1 + exp(-lp[i,j]))
      p.eff[i, j] \leftarrow z[i] * p[i,j]
      y[i, j] \sim dbern(p.eff[i,j])
    }
  N0 < - sum(z[])
  Insert the proportion of identifiable individual section here.
  Ntotal <- N0/mean.p2
Mtb:
model {
  # priors
  Omega \sim dunif(0, 1)
  for (j in 1:J){
    p[j] \sim dunif(0, 1)
    c[j] \sim dunif(0, 1)
  # likelihood
    for (i in 1:I){
    z[i] ~ dbern(Omega)
```

Appendix 1 continued.

```
# first occasion
    yaug[i, 1] \sim dbern(p.eff[i,1])
   p.eff[i,1] \leftarrow z[i] * p[1]
    for (j in 2:J){
      yaug[i, j] ~ dbern(p.eff[i,j])
       p.eff[i, j] <- z[i] * ((1 - yaug[i, (j-1)]) * p[j] + yaug[i, (j-1)] * c[j] ) 
  }
  N0 <- sum(z[])
  Insert the proportion of identifiable individual section here.
 Ntotal <- N0/mean.p2</pre>
}
M_{tbh}:
model {
  # priors
  Omega \sim dunif(0, 1)
  for (j in 1:J){
   mean.lp[j] <- log(mean.p[j] / (1 - mean.p[j])) #logit(p)</pre>
   mean.p[j] ~ dunif(0, 1) # detection intercepts
  gamma \sim dnorm(0, 0.1)
  # changed sd and tau definition to see if
  # defining a prior on tau may help convergence
  tau ~ dgamma(5, 1)
  sd <- 1/sqrt(tau)</pre>
  # likelihood
  for (i in 1:I){
    z[i] \sim dbern(Omega)
    eps[i] ~ dnorm(0, tau) # jags doesn't like I(L,U)
    # first occasion: no term for recapture
   y[i,1] \sim dbern(p.eff[i,1])
   p.eff[i,1] \leftarrow z[i] * p[i, 1]
   p[i, 1] \leftarrow 1/(1 + exp(-lp[i,1]))
    lp[i, 1] \leftarrow mean.lp[1] + eps[i]
    # subsequent occasions: include recapture
    for (j in 2:J){
      y[i, j] \sim dbern(p.eff[i,j])
      p.eff[i, j] \leftarrow z[i] * p[i,j]
      p[i,j] \leftarrow 1 / (1 + exp(-lp[i,j]))
      lp[i,j] \leftarrow mean.lp[j] + eps[i] + gamma * y[i, (j-1)]
  N0 <- sum(z[])
  Insert the proportion of identifiable individual section here.
 Ntotal <- N0/mean.p2
}
```

Appendix 2. R code used to run M0 model above. Other models use similar R code, in which model name, data structure, and initial value function are modified according to each model.

```
rm(list=ls())
library(rjags)
SAVE <- TRUE
runDate <- Sys.Date()</pre>
tBegin <- Sys.time()</pre>
## set MCMC parameters
n.adapt <- 100000
n.update <- 100000
n.iter <- 100000
n.chains <- 5
ModelName <- "Model_M0_M9.txt"</pre>
if (SAVE == TRUE) saveFname <- paste("M0_M9_",</pre>
                                        runDate, "Max.RData",
                                         sep = "")
# first get data:
file01 <- 'ResightsMax01_05182014.csv'
data01 <- read.table(file = file01, header = FALSE, sep = ",")</pre>
nGrp <- 41
nObs <- 2
maxIndiv <- 29
Kvec <- as.vector(read.csv('Kvec.csv',</pre>
                             header = FALSE), mode = "numeric")
Kvec[is.na(Kvec)] <- 0</pre>
Kmat <- matrix(data = Kvec,</pre>
                nrow = nGrp, ncol = nObs,
                byrow = FALSE)
Kvec2 <- apply(Kmat, 1, sum)</pre>
Nvec <- as.vector(read.csv('Nvec.csv',</pre>
                             header = FALSE), mode = "numeric")
Nvec[is.na(Nvec)] <- 0</pre>
Nmat <- matrix(data = Nvec,</pre>
                nrow = nGrp, ncol = nObs,
                byrow = FALSE)
Nvec2 <- apply(Nmat, 1, sum)</pre>
Mvec <- as.vector(read.csv('Mvec.csv',</pre>
                             header = FALSE), mode = "numeric")
Mmat <- matrix(data = Mvec,</pre>
                nrow = nGrp, ncol = nObs,
                byrow = FALSE)
Mvec2 <- apply(Mmat, 1, max)</pre>
Yvec <- as.vector(read.csv('Yvec.csv',
                             header = FALSE), mode = "numeric")
Yvec[is.na(Yvec)] <- 0
Ymat <- matrix(data = Yvec,
                nrow = nGrp, ncol = nObs,
                byrow = FALSE)
Yvec2 <- apply(Ymat, 1, sum)
kMat <- as.matrix(read.csv('kArray.csv',</pre>
                             header = FALSE))
```

Appendix 2 continued.

```
kMat[is.na(kMat)] <- 0</pre>
kArray <- array(data = as.vector(t(kMat), mode = "numeric"),</pre>
                  dim = c(maxIndiv, nGrp, nObs))
kMat1 <- kArray[,,1] + kArray[,,2]</pre>
kMat01 <- matrix(data = 0, nrow = dim(kMat1)[1], ncol = dim(kMat1)[2])</pre>
kMat01[kMat1 > 0] <- 1
xVec <- apply(kMat01, 2, sum)</pre>
Tvec <- Kvec2 + Yvec2
Tmat <- matrix(data = Tvec,</pre>
                nrow = nGrp,
                ncol = nObs,
                byrow = FALSE)
params = c("mean.p", "s", "deviance",
            "p", "N0",
            "p2", "Omega", "Ntotal")
# Augment data
nz <- 600
yobs <- as.matrix(data01)</pre>
yaug <- rbind(yobs, array(0, dim = c(nz, dim(yobs)[2])))</pre>
bugs.dat <- list(yaug = yaug,</pre>
                  G = nGrp,
                  I = nrow(yaug),
                  J = ncol(yaug),
                  N = Nvec2,
                  K = Kvec2,
                  T = Tvec,
                  x = xVec,
                  M = Mvec2
                  k = kMat1,
                  pi = rep(0.02, times = 50))
inits.func <- function(){ list(s = runif(1, 1, 3),</pre>
                                 mean.p = runif(1, 0.8, 1),
                                 z = rep(1, nrow(yaug)),
                                 p = runif(1, 0, 1))
jm <- jags.model(ModelName,</pre>
                  data = bugs.dat,
                  inits = inits.func,
                  n.chains = n.chains,
                  n.adapt = n.adapt)
update(jm, n.iter = n.update)
load.module("dic")
zm <- coda.samples(jm,</pre>
                    variable.names = params,
                    n.iter = n.iter)
g.diag <- gelman.diag(zm, multivariate = FALSE)</pre>
h.diag <- heidel.diag(zm)</pre>
r.diag <- raftery.diag(zm)</pre>
tEnd <- Sys.time()
if (SAVE == TRUE) save(list = ls(all = TRUE), file = saveFname)
```